

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of the Claims

1. – 9. (Cancelled).

10. (Currently Amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginy) beta-hydroxylase (AAH), wherein said compound is a ~~AAH-antisense~~ nucleic acid comprising a an antisense sequence which is complementary to a 5' AAH regulatory sequence of SEQ ID NO:3, said antisense sequence ~~nucleic acid~~ consisting of ~~between 10-50 nucleotides, inclusive,~~ in length and wherein said tumor overexpresses AAH compared to a normal noncancerous ~~cell~~ cells.

11. – 12. (Cancelled).

13. (Original) The method of claim 10, wherein said tumor is derived from endodermal tissue.

14. (Original) The method of claim 10, wherein said tumor is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer, and cancer of the bile ducts.

15. (Original) The method of claim 10, wherein said tumor is a CNS tumor.

16. – 38. (Cancelled).

39. (Previously Presented) The method of claim 10, wherein said tumor is a glioblastoma.

40. (Previously Presented) The method of claim 10, wherein said tumor is a neuroblastoma.

41. (Previously Presented) The method of claim 10, wherein said tumor is a cholangiocarcinoma.

42. (Previously Presented) The method of claim 10, wherein said tumor is a hepatocellular carcinoma.

43. (Currently Amended) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a ~~HAAH-antisense~~ nucleic acid, wherein said nucleic acid comprises a an antisense sequence which is complementary to a 5' portion of an AAH coding sequence of SEQ ID-~~NO:2~~ NO:3 and comprises a sequence complementary to the initiating ATG methionine-encoding codon of said SEQ ID NO:3, said antisense sequence ~~nucleic acid~~ consisting of between 10-50 nucleotides, inclusive, in length and wherein said tumor overexpresses AAH compared to a normal

noncancerous ~~cell~~ cells.

44. (Previously Presented) The method of claim 43, wherein said tumor is derived from endodermal tissue.

45. (Previously Presented) The method of claim 43, wherein said tumor is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer, and cancer of the bile ducts.

46. (Previously Presented) The method of claim 43, wherein said tumor is a CNS tumor.

47. (Previously Presented) The method of claim 43, wherein said tumor is a glioblastoma.

48. (Previously Presented) The method of claim 43, wherein said tumor is a neuroblastoma.

49. (Previously Presented) The method of claim 43, wherein said tumor is a cholangiocarcinoma.

50. (Previously Presented) The method of claim 43, wherein said tumor is a hepatocellular carcinoma.

51. – 71. (Cancelled).

72. (Currently Amended) ~~The method of claim 10~~ A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginy) beta-hydroxylase (AAH), wherein said compound is a nucleic acid comprising a an antisense sequence which is complementary to a 5' AAH regulatory sequence of SEQ ID NO:3, wherein said tumor overexpresses AAH compared to a normal noncancerous cells, and wherein the length of said antisense ~~nucleic acid~~ sequence consists of between 10 – 20 nucleotides, inclusive.

73. (Currently Presented) The method of claim 43, wherein the length of said antisense ~~nucleic acid~~ sequence consists of between 10 –20 nucleotides, inclusive.

74. (New) A method of inhibiting tumor growth in a mammal, comprising administering to said mammal a compound which inhibits expression of alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginy) beta-hydroxylase (AAH), wherein said compound is a nucleic acid comprising a an antisense sequence which is complementary to a 5' AAH regulatory sequence of SEQ ID NO:3, wherein said tumor overexpresses AAH compared to a normal noncancerous cells, wherein said antisense sequence consists of between 10-50 nucleotides in length, inclusive, and comprises a portion that is complementary to a 5' coding region of SEQ ID NO:3 which includes the ATG initiating methionine-encoding codon.

75. (New) The method of claim 74, wherein said antisense sequence consists of between 10–20 nucleotides in length, inclusive.

76. (New) The method of claim 10 or claim 43, wherein said mammal is human.